RAW SEQUENCE LISTING
ERROR REPORT

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Application Serial Number: *10/547,532*

Source: *PCT/10*

Date Processed by STIC: *9/13/05*

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2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
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1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , **EFS Submission User Manual** - ePAVE)
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Revised 01/24/05

PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/547,532

DATE: 09/13/2005
TIME: 13:24:41

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\09132005\J547532.raw**

pp 1-10

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      3 <110> APPLICANT: SHINTANI, ET AL.
      5 <120> TITLE OF INVENTION: MEDICINAL USE OF MIP-3a INHIBITOR AND METHOD OF SCREENING
BRAIN/NERVE
      6       CELL PROTECTIVE AGENT
      8 <130> FILE REFERENCE: 20039.1USWO
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/547,532
C--> 11 <141> CURRENT FILING DATE: 2005-08-31
     13 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/002774
     14 <151> PRIOR FILING DATE: 2004-03-04
     16 <150> PRIOR APPLICATION NUMBER: JP 2003-056885
     17 <151> PRIOR FILING DATE: 2003-03-04
     19 <150> PRIOR APPLICATION NUMBER: JP 2003-106247
     20 <151> PRIOR FILING DATE: 2003-04-10
     22 <160> NUMBER OF SEQ ID NOS: 21
     24 <170> SOFTWARE: PatentIn version 3.1
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Suggestion: Consult Sequence Rules for valid format

Does Not Comply Corrected Diskette Needed

Cumulative base totals are at right margin of each line.

ERRORED SEQUENCES

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     26 <210> SEQ ID NO: 1
     27 <211> LENGTH: 288
     28 <212> TYPE: DNA
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     33 <222> LOCATION: (1)..(288)
     34 <223> OTHER INFORMATION:
     36 <220> FEATURE:
     37 <221> NAME/KEY: sig_peptide
     38 <222> LOCATION: (1)..(78)
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W--> 41 <220>
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     43 <222> LOCATION: (79)..()
     44 <223> OTHER INFORMATION:
W--> 46 <400> 1
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Amino acid numbers are completely misaligned

Insert a hard return. Amino acids go directly under their codons.

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W--> 47 atg tgc tgt acc aag agt ttg ctc ctg gct gct ttg atg tca gtg ctg        48Met Cys
E--> 48 Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu              -25
W--> 49 -20               -15                          cta ctc cac ctc tgc ggc gaa tca
W--> 50 gaa gca gca agc aac ttt gac tgc        96Leu Leu His Leu Cys Gly Glu Ser Glu Ala
E--> 51 ala ser asn Phe asp cys        -10              -5                    -1 1
W--> 52 5              tgt ctt gga tac aca gac cgt att ctt cat cct aaa ttt att gtg ggc
W--> 53 144Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly
W--> 54 10               15                 20               ttc aca cgg cag ctg
```

invalid format

```
                    RAW SEQUENCE LISTING            DATE: 09/13/2005
                    PATENT APPLICATION:  US/10/547,532    TIME: 13:24:41

                    Input Set : A:\PTO.AMC.txt
                    Output Set: N:\CRF4\09132005\J547532.raw
```

```
W--> 55 gcc aat gaa ggc tgt gac atc aat gct atc atc        192Phe Thr Arg Gln Leu Ala Asn
E--> 56 glu gly cys asp Ile asn ala Ile Ile                   25                30
W--> 57 35                         ttt cac aca aag aaa aag ttg tct gtg tgc gca aat cca aaa
W--> 58 cag act         240Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
W--> 59      40               45                    50                       tgg gtg
W--> 60 aaa tat att gtg cgt ctc ctc agt aaa aaa gtc aag aac atg        288Trp Val Lys Tyr
E--> 61 Ile val arg Leu Leu ser Lys Lys val Lys asn met           55            60
E--> 62 65                   70
     83 <210> SEQ ID NO: 3
     84 <211> LENGTH: 288
     85 <212> TYPE: DNA
     86 <213> ORGANISM: Rattus norvegicus
     88 <220> FEATURE:
     89 <221> NAME/KEY: CDS
     90 <222> LOCATION: (1)..(288)
     91 <223> OTHER INFORMATION:
     93 <220> FEATURE:
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W--> 98 <220>
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E--> 105 cys Lys his Leu Pro Phe Leu ala Leu ala gly val Leu Leu              -25
E--> 106 -20                 -15                  -10
W--> 107 gct tac ctc tgc agc cag tca gaa gca gca agc aac ttt gac tgc tgc        96Ala Tyr
W--> 108 Leu Cys Ser Gln Ser Glu Ala Ala Ser Asn Phe Asp Cys Cys
W--> 109 -5                 -1 1                5              ctc acg tac aca aag aac
W--> 110 gtg tat cat cat gcg aga aat ttt gtg ggt        144Leu Thr Tyr Thr Lys Asn Val Tyr
E--> 111 his his ala arg asn Phe val gly                  10                 15
W--> 112 20              ttc aca aca cag atg gcc gac gaa gct tgt gac att aat gct
W--> 113 atc atc        192Phe Thr Thr Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile Ile
W--> 114 25                  30                  35                       ttt cac ctg
W--> 115 aag tcg aaa aga tcc gtg tgc gct gac cca aag cag atc        240Phe His Leu Lys Ser
E--> 116 Lys arg ser val cys ala asp Pro Lys gln Ile            40                45
W--> 117 50                  55          tgg gtg aaa agg att ttg cac ctc ctc agc cta aga
W--> 118 acc aag aag atg        288Trp Val Lys Arg Ile Leu His Leu Leu Ser Leu Arg Thr Lys
E--> 119 Lys met                60              65                70
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    143 <213> ORGANISM: Mus musculus
    145 <220> FEATURE:
    146 <221> NAME/KEY: CDS
    147 <222> LOCATION: (1)..(291)
    148 <223> OTHER INFORMATION:
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Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\09132005\J547532.raw**

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      151 <221> NAME/KEY: sig_peptide
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      153 <223> OTHER INFORMATION:
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      156 <221> NAME/KEY: mat_peptide
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E-->  162 cys gly gly Lys arg Leu Leu Phe Leu ala Leu ala trp val                   -25
W-->  163 -20                     -15                 ctg ctg gct cac ctc tgc agc cag gca
W-->  164 gaa gca gca agc aac tac gac        96Leu Leu Ala His Leu Cys Ser Gln Ala Glu Ala
E-->  165 ala ser asn tyr asp               -10              -5              -1   1
W-->  166 5               tgt tgc ctc tcg tac ata cag acg cct ctt cct tcc aga gct att gtg
W-->  167 144Cys Cys Leu Ser Tyr Ile Gln Thr Pro Leu Pro Ser Arg Ala Ile Val
W-->  168 10                15                 20                ggt ttc aca aga cag atg
W-->  169 gcc gat gaa gct tgt gac att aat gct atc        192Gly Phe Thr Arg Gln Met Ala Asp
E-->  170 glu ala cys asp Ile asn ala Ile                     25                30
W-->  171 35               atc ttt cac acg aag aaa aga aaa tct gtg tgc gct gat cca aag
W-->  172 cag        240Ile Phe His Thr Lys Lys Arg Lys Ser Val Cys Ala Asp Pro Lys Gln
W-->  173 40                45                 50                aac tgg gtg aaa
W-->  174 agg gct gtg aac ctc ctc agc cta aga gtc aag aag        288Asn Trp Val Lys Arg Ala
E-->  175 val asn Leu Leu ser Leu arg val Lys Lys               55                60
W-->  176 65                      atg
E-->  177 291met                                                                 70
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      203 <213> ORGANISM: Homo sapiens
      205 <220> FEATURE:
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      208 <223> OTHER INFORMATION:
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E-->  212 gly glu ser met asn Phe ser asp val Phe asp ser ser glu        1
W-->  213 5                     10                 15                gat tat ttt gtg tca gtc
W-->  214 aat act tca tat tac tca gtt gat tct gag        96Asp Tyr Phe Val Ser Val Asn Thr
E-->  215 ser tyr tyr ser val asp ser glu                     20                25
W-->  216 30                atg tta ctg tgc tcc ttg cag gag gtc agg cag ttc tcc agg cta
W-->  217 ttt        144Met Leu Leu Cys Ser Leu Gln Glu Val Arg Gln Phe Ser Arg Leu Phe
W-->  218 35                40                 45                gta ccg att gcc
W-->  219 tac tcc ttg atc tgt gtc ttt ggc ctc ctg ggg aat        192Val Pro Ile Ala Tyr Ser
E-->  220 Leu Ile cys val Phe gly Leu Leu gly asn               50                55
W-->  221 60                att ctg gtg gtg atc acc ttt gct ttt tat aag aag gcc
W-->  222 agg tct atg        240Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser
E-->  223 met          65                 70                 75                80
W-->  224 aca gac gtc tat ctc ttg aac atg gcc att gca gac atc ctc ttt gtt        288Thr Asp
```

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```
W--> 225 Val Tyr Leu Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val    same
W--> 226 85                  90              95            ctt act ctc cca ttc tgg
W--> 227 gca gtg agt cat gcc act ggt gcg tgg gtt    336Leu Thr Leu Pro Phe Trp Ala Val
E--> 228 ser his ala thr gly ala trp val            100                     105
W--> 229 110                 ttc agc aat gcc acg tgc aag ttg cta aaa ggc atc tat gcc atc
W--> 230 aac        384Phe Ser Asn Ala Thr Cys Lys Leu Leu Lys Gly Ile Tyr Ala Ile Asn
W--> 231 115                120                  125             ttt aac tgc ggg
W--> 232 atg ctg ctc ctg act tgc att agc atg gac cgg tac    432Phe Asn Cys Gly Met Leu
E--> 233 Leu Leu thr cys Ile ser met asp arg tyr           130                   135
W--> 234 140              atc gcc att gta cag gcg act aag tca ttc cgg ctc cga
W--> 235 tcc aga aca        480Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Leu Arg Ser Arg
E--> 236 thr        145                150                 155                  160
W--> 237 cta ccg cgc agc aaa atc atc tgc ctt gtt gtg tgg ggg ctg tca gtc      528Leu Pro
W--> 238 Arg Ser Lys Ile Ile Cys Leu Val Val Trp Gly Leu Ser Val
W--> 239 165                170                 175             atc atc tcc agc tca act
W--> 240 ttt gtc ttc aac caa aaa tac aac acc caa    576Ile Ile Ser Ser Ser Thr Phe Val
E--> 241 Phe asn gln Lys tyr asn thr gln           180                     185
W--> 242 190              ggc agc gat gtc tgt gaa ccc aag tac cag act gtc tcg gag ccc
W--> 243 atc        624Gly Ser Asp Val Cys Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile
W--> 244 195                200                 205             agg tgg aag ctg
W--> 245 ctg atg ttg ggg ctt gag cta ctc ttt ggt ttc ttt    672Arg Trp Lys Leu Leu Met
E--> 246 Leu gly Leu glu Leu Leu Phe gly Phe Phe           210                   215
W--> 247 220              atc cct ttg atg ttc atg ata ttt tgt tac acg ttc att
W--> 248 gtc aaa acc        720Ile Pro Leu Met Phe Met Ile Phe Cys Tyr Thr Phe Ile Val Lys
E--> 249 thr        225                230                 235                  240
W--> 250 ttg gtg caa gct cag aat tct aaa agg cac aaa gcc atc cgt gta atc      768Leu Val
W--> 251 Gln Ala Gln Asn Ser Lys Arg His Lys Ala Ile Arg Val Ile
W--> 252 245                250                 255             ata gct gtg gtg ctt gtg
W--> 253 ttt ctg gct tgt cag att cct cat aac atg    816Ile Ala Val Val Leu Val Phe Leu
E--> 254 ala cys gln Ile Pro his asn met           260                     265
W--> 255 270              gtc ctg ctt gtg acg gct gca aat ttg ggt aaa atg aac cga tcc
W--> 256 tgc        864Val Leu Leu Val Thr Ala Ala Asn Leu Gly Lys Met Asn Arg Ser Cys
W--> 257 275                280                 285             cag agc gaa aag
W--> 258 cta att ggc tat acg aaa act gtc aca gaa gtc ctg    912Gln Ser Glu Lys Leu Ile
E--> 259 gly tyr thr Lys thr val thr glu val Leu           290                   295
W--> 260 300              gct ttc ctg cac tgc tgc ctg aac cct gtg ctc tac gct
W--> 261 ttt att ggg        960Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile
E--> 262 gly        305                310                 315                  320
W--> 263 cag aag ttc aga aac tac ttt ctg aag atc ttg aag gac ctg tgg tgt      1008Gln Lys
W--> 264 Phe Arg Asn Tyr Phe Leu Lys Ile Leu Lys Asp Leu Trp Cys
W--> 265 325                330                 335             gtg aga agg aag tac aag
W--> 266 tcc tca ggc ttc tcc tgt gcc ggg agg tac    1056Val Arg Arg Lys Tyr Lys Ser Ser
E--> 267 gly Phe ser cys ala gly arg tyr           340                     345
W--> 268 350              tca gaa aac att tct cgg cag acc agt gag acc gca gat aac gac
W--> 269 aat        1104Ser Glu Asn Ile Ser Arg Gln Thr Ser Glu Thr Ala Asp Asn Asp Asn
W--> 270 355                360                 365             gcg tcg tcc ttc
W--> 271 act atg                                             1122Ala Ser Ser Phe Thr Met
E--> 272 370
     329 <210> SEQ ID NO: 9
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PATENT APPLICATION: US/10/547,532

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Input Set : A:\PTO.AMC.txt
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      336  <222> LOCATION: (1)..(1101)
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W-->  342  5                       10                      15          gag tat tat tct att cct
W-->  343  cca gac cat ggg cca tgc tcc cta gaa gag          96Glu Tyr Tyr Ser Ile Pro Pro Asp
E-->  344  his gly Pro cys ser Leu glu glu          20                      25
W-->  345  30                      gtc aga aac ttc acc aag gta ttt gtg cca att gcc tac tcc tta
W-->  346  ata          144Val Arg Asn Phe Thr Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile
W-->  347  35                      40                      45          tgt gtc ttt ggc
W-->  348  ctc ctg ggc aac att atg gtg gtg atg acc ttt gcc          192Cys Val Phe Gly Leu Leu
E-->  349  gly asn Ile met val val met thr Phe ala          50                      55
W-->  350  60                      ttc tac aag aaa gcc aga tcc atg act gac gtc tac ctg
W-->  351  ttg aac atg          240Phe Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn
E-->  352  met          65                      70                      75          80
W-->  353  gcc atc aca gac ata ctc ttt gtc ctc acc cta ccg ttc tgg gca gtt          288Ala Ile
W-->  354  Thr Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val
W-->  355  85                      90                      95          act cat gcc acc aac act
W-->  356  tgg gtt ttc agc gat gca ctg tgt aaa ctg          336Thr His Ala Thr Asn Thr Trp Val
E-->  357  Phe ser asp ala Leu cys Lys Leu          100                      105
W-->  358  110                     atg aaa ggc aca tat gcg gtc aac ttt aac tgt ggg atg ctg ctc
W-->  359  ctg          384Met Lys Gly Thr Tyr Ala Val Asn Phe Asn Cys Gly Met Leu Leu Leu
W-->  360  115                     120                     125          gcc tgt atc agc
W-->  361  atg gac cgg tac att gcc atc gtc cag gca acc aaa          432Ala Cys Ile Ser Met Asp
E-->  362  arg tyr Ile ala Ile val gln ala thr Lys          130                      135
W-->  363  140                     tct ttc cgg gta cgc tcc aga aca ctg acg cac agt aag
W-->  364  gtc atc tgt          480Ser Phe Arg Val Arg Ser Arg Thr Leu Thr His Ser Lys Val Ile
E-->  365  cys          145                     150                     155          160
W-->  366  gtg gca gtg tgg ttc atc tcc atc atc atc tca agc cct aca ttt atc          528Val Ala
W-->  367  Val Trp Phe Ile Ser Ile Ile Ile Ser Ser Pro Thr Phe Ile
W-->  368  165                     170                     175          ttc aac aag aaa tac gag
W-->  369  ctg cag gat cgt gat gtc tgt gag cca cgg          576Phe Asn Lys Lys Tyr Glu Leu Gln
E-->  370  asp arg asp val cys glu Pro arg          180                      185
W-->  371  190                     tac agg tct gtc tca gag ccc atc acg tgg aag ctg ctg ggt atg
W-->  372  gga          624Tyr Arg Ser Val Ser Glu Pro Ile Thr Trp Lys Leu Leu Gly Met Gly
W-->  373  195                     200                     205          ctg gag ctg ttc
W-->  374  ttt ggg ttc ttc acc cct ttg ctg ttt atg gtg ttc          672Leu Glu Leu Phe Phe Gly
E-->  375  Phe Phe thr Pro Leu Leu Phe met val Phe          210                      215
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W-->  377  aac tcc aag          720Cys Tyr Leu Phe Ile Ile Lys Thr Leu Val Gln Ala Gln Asn Ser
E-->  378  Lys          225                     230                     235          240
W-->  379  agg cac aga gcc atc cga gtc gtg atc gct gtg gtt ctc gtg ttc ctg          768Arg His
W-->  380  Arg Ala Ile Arg Val Val Ile Ala Val Val Leu Val Phe Leu
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W--> 381 245              250              255           gct tgt cag atc cct cac
W--> 382 aac atg gtc ctc ctc gtg act gcg gtc aac      816Ala Cys Gln Ile Pro His Asn Met
E--> 383 val Leu Leu val thr ala val asn              260              265
W--> 384 270              acg ggc aaa gtg ggc cgg agc tgc agc acc gag aaa gtc ctc gcc
W--> 385 tac       864Thr Gly Lys Val Gly Arg Ser Cys Ser Thr Glu Lys Val Leu Ala Tyr
W--> 386 275              280              285              acc agg aac gtg
W--> 387 gcc gag gtc ctg gct ttc ctg cat tgc tgc ctc aac      912Thr Arg Asn Val Ala Glu
E--> 388 val Leu ala Phe Leu his cys cys Leu asn              290              295
W--> 389 300              ccc gtg ttg tat gcg ttt att gga cag aaa ttc aga aac
W--> 390 tac ttc atg       960Pro Val Leu Tyr Ala Phe Ile Gly Gln Lys Phe Arg Asn Tyr Phe
E--> 391 met       305              310              315              320
W--> 392 aag atc atg aag gat gtg tgg tgt atg aga agg aag aat aag atg cct       1008Lys Ile
W--> 393 Met Lys Asp Val Trp Cys Met Arg Arg Lys Asn Lys Met Pro
W--> 394 325              330              335           ggc ttc ctc tgt gcc cgg
W--> 395 gtt tac tcg gaa agc tac atc tcc agg cag      1056Gly Phe Leu Cys Ala Arg Val Tyr
E--> 396 ser glu ser tyr Ile ser arg gln              340              345
W--> 397 350              acc agt gag acc gtc gaa aat gat aat gca tcg tcc ttt acc atg
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W--> 493 120acacctgcag tttgaagtca tcactttcaa tcccctgtg actagggcca gggtcttcac
W--> 494 180acctgcgaga ggaagcaaag atctaagcaa tctgaatttt aagagagaaa ctgcagctgt
W--> 495 240cggtttgtgg gccggaacat tattggactg gagcctggac aagcactaag gcggggggtac
E--> 496 300ctggccagcc cacttcggag ctcagcgttt ccttgggaaa cg atg aat ttc acc       354
E--> 497 met asn Phe thr              1
W--> 498 gag gcc aac tac gga atg gaa gat tat act ggc tca gat tac tct atg       402Glu Ala
E--> 499 asn tyr gly met glu asp tyr thr gly ser asp tyr ser met       5
W--> 500 10              15              20           ttt cca gag acc gag cca tgc
W--> 501 tct ctg caa gag gtc aga gac ttc acc       450Phe Pro Glu Thr Glu Pro Cys Ser Leu
E--> 502 gln glu val arg asp Phe thr              25              30
W--> 503 35              aag gtg ttc gtg cca atc gcc tac tcc tta atc tgt gtc ttt ggc ctc
W--> 504 498Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu
W--> 505 40              45              50           ctt ggc aat att atg
W--> 506 gtg gtg ata acc ttt gcc ttc tac aag aaa gcc       546Leu Gly Asn Ile Met Val Val
E--> 507 Ile thr Phe ala Phe tyr Lys Lys ala              55              60
W--> 508 65              agg tcc atg act gac gtc tac cta ttg aac atg gcc atc aca
W--> 509 gac ata       594Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Thr Asp Ile
W--> 510 70              75              80           ctc ttt gtc
W--> 511 ctc acc cta cca ttc tgg gca gtt act cat gcc act gac       642Leu Phe Val Leu Thr
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Cumulative base totals are at right margin of each line (handwritten annotation)

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         RAW SEQUENCE LISTING               DATE: 09/13/2005
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         Input Set : A:\PTO.AMC.txt
         Output Set: N:\CRF4\09132005\J547532.raw
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E--> 512 Leu Pro Phe trp ala val thr his ala thr asp      85              90
W--> 513 95              100        act tgg atc ttt ggc aac acg atg tgt aaa ctg atg
W--> 514 aaa ggc acg tat      690Thr Trp Ile Phe Gly Asn Thr Met Cys Lys Leu Met Lys Gly
E--> 515 thr tyr                 105              110              115
W--> 516 gcg gtc aac ttt aac tgt ggg atg ctg ctc ctg gcc tgt atc agc atg      738Ala Val
E--> 517 asn Phe asn cys gly met Leu Leu Leu ala cys Ile ser met              120
W--> 518 125              130        gac cgg tac att gcc atc gtc cag gcg acc
W--> 519 aaa tct ttc cgg gta cgc      786Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys Ser
E--> 520 Phe arg val arg                 135              140              145
W--> 521 tcc aga aca ctg acg cac agt aag gtc atc tgt ctg acg gtg tgg ttc      834Ser Arg
E--> 522 thr Leu thr his ser Lys val Ile cys Leu thr val trp Phe              150
W--> 523 155              160        gtt tcc atc atc atc tca agc ccc
W--> 524 aca ttc ttc ttc aac aag caa tac      882Val Ser Ile Ile Ile Ser Ser Pro Thr Phe
E--> 525 Phe Phe asn Lys gln tyr      165              170              175
W--> 526 180        aag ctg cag ggc cgt gat gtc tgc gag cct cag tac aag ctc gtc tcg
W--> 527 930Lys Leu Gln Gly Arg Asp Val Cys Glu Pro Gln Tyr Lys Leu Val Ser
W--> 528 185              190              195        gag ccc atc acg tgg aaa
W--> 529 ctg ctg ggc atg gga ctc gag ctg ctc ttt      978Glu Pro Ile Thr Trp Lys Leu Leu
E--> 530 gly met gly Leu glu Leu Leu Phe              200              205
W--> 531 210        ggc ttc ttc atc cct ttg ctg ttt atg gtg ttc tgt tac ctg ttc
W--> 532 atc      1026Gly Phe Phe Ile Pro Leu Leu Phe Met Val Phe Cys Tyr Leu Phe Ile
W--> 533 215              220              225        atc aag acc ttg
W--> 534 gtg cag gcc cag aat tcc aag agg cac aga gcc atc      1074Ile Lys Thr Leu Val Gln
E--> 535 ala gln asn ser Lys arg his arg ala Ile              230              235
W--> 536 240        cga gtc gtg att gct gtg gtt ctc gtg ttc ctg gct tgt
W--> 537 cag atc cct      1122Arg Val Val Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile
E--> 538 Pro      245              250              255              260
W--> 539 cac aac atg gtc ctc ctc gtg act gca gcc aac acg ggc aaa atg ggc      1170His Asn
W--> 540 Met Val Leu Leu Val Thr Ala Ala Asn Thr Gly Lys Met Gly
W--> 541 265              270              275        cgc agc tgc agc gcc gag
W--> 542 aaa gcc ctc gcc tac gcc agg aat gtg gct      1218Arg Ser Cys Ser Ala Glu Lys Ala
E--> 543 Leu ala tyr ala arg asn val ala              280              285
W--> 544 290        gag gtc ctg gct ttc ctg cac tgc tgt ctc aac ccc gtg ttg tat
W--> 545 gcc      1266Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala
W--> 546 295              300              305        ttc att gga cag
W--> 547 aaa ttc aga agc tac ttc atg aag atc atg aag gat      1314Phe Ile Gly Gln Lys Phe
E--> 548 arg ser tyr Phe met Lys Ile met Lys asp              310              315
W--> 549 320        gtg tgg tgt atg agg agg aag agc aag gtg cct acc ttc
W--> 550 ttc tgt gcc      1362Val Trp Cys Met Arg Arg Lys Ser Lys Val Pro Thr Phe Phe Cys
E--> 551 ala      325              330              335              340
W--> 552 cgg gtt tac tca gaa agc tac atc tcc agg cag acc agt gag act gta      1410Arg Val
W--> 553 Tyr Ser Glu Ser Tyr Ile Ser Arg Gln Thr Ser Glu Thr Val
W--> 554 345              350              355        gaa aat gac aac gca tcg
W--> 555 tcc ttt acc atg taa cacgagagca caaagcagca      1463Glu Asn Asp Asn Ala Ser Ser Phe
E--> 556 thr met                 360              365
E--> 557 tgccccgaaa gcctttgtga aacttgctat tacatgtga      1502
     612 <210> SEQ ID NO: 15
     613 <211> LENGTH: 1309
     614 <212> TYPE: DNA
```

RAW SEQUENCE LISTING   DATE: 09/13/2005
PATENT APPLICATION: US/10/547,532   TIME: 13:24:41

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\09132005\J547532.raw**

```
      615 <213> ORGANISM: Rattus norvegicus (liver)
      617 <220> FEATURE:
      618 <221> NAME/KEY: CDS
      619 <222> LOCATION: (150)..(1250)
      620 <223> OTHER INFORMATION:
W-->  622 <400> 15
E-->  623 gcatctcact acccgtctct caatgagcac cgctggttgt gcctgtcaac agaatagtcc
W-->  624 60tctcacactt aggactggag cctggacaag cactaaggcg ggggtacctg gccagcccac
E-->  625 120ttcggagctc agcgtttcct tgggaaacg atg aat ttc acc gag gcc aac tac      173
E-->  626 met asn Phe thr glu ala asn tyr                                        1
W-->  627 5                 gga atg gaa gat tat act ggc tca gat tac tct atg ttt cca
W-->  628 gag acc      221Gly Met Glu Asp Tyr Thr Gly Ser Asp Tyr Ser Met Phe Pro Glu Thr
W-->  629 10               15                20                    gag cca tgc
W-->  630 tct ctg caa gag gtc aga gac ttc acc aag gtg ttc gtg      269Glu Pro Cys Ser Leu
E-->  631 gln glu val arg asp Phe thr Lys val Phe val      25                30
W-->  632 35             40             cca atc gcc tac tcc tta atc tgt gtc ttt ggc ctc
W-->  633 ctt ggc aat att      317Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly
E-->  634 asn Ile               45                50                55
W-->  635 atg gtg gtg ata acc ttt gcc ttc tac aag aaa gcc agg tcc atg act      365Met Val
E-->  636 val Ile thr Phe ala Phe tyr Lys Lys ala arg ser met thr                60
W-->  637 65             70             gac gtc tac cta ttg aac atg gcc atc aca
W-->  638 gac ata ctc ttt gtc ctc      413Asp Val Tyr Leu Leu Asn Met Ala Ile Thr Asp Ile
E-->  639 Leu Phe val Leu               75                80                85
W-->  640 acc cta cca ttc tgg gca gtt act cat gcc act gac act tgg atc ttt      461Thr Leu
E-->  641 Pro Phe trp ala val thr his ala thr asp thr trp Ile Phe                90
W-->  642 95             100             ggc aac acg atg tgt aaa ctg atg
W-->  643 aaa ggc acg tat gcg gtc aac ttt      509Gly Asn Thr Met Cys Lys Leu Met Lys Gly
E-->  644 thr tyr ala val asn Phe      105                110                115
W-->  645 120         aac tgt ggg atg ctg ctc ctg gcc tgt atc agc atg gac cgg tac att
W-->  646 557Asn Cys Gly Met Leu Leu Leu Ala Cys Ile Ser Met Asp Arg Tyr Ile
W-->  647 125             130             135         gcc atc gtc cag gcg acc
W-->  648 aaa tct ttc cgg gta cgc tcc aga aca ctg      605Ala Ile Val Gln Ala Thr Lys Ser
E-->  649 Phe arg val arg ser arg thr Leu      140                145
W-->  650 150             acg cac agt aag gtc atc tgt ctg acg gtg tgg ttc gtt tcc atc
W-->  651 atc      653Thr His Ser Lys Val Ile Cys Leu Thr Val Trp Phe Val Ser Ile Ile
W-->  652 155             160             165         atc tca agc ccc
W-->  653 aca ttc ttc ttc aac aag caa tac aag ctg cag ggc      701Ile Ser Ser Pro Thr Phe
E-->  654 Phe Phe asn Lys gln tyr Lys Leu gln gly      170                175
W-->  655 180             cgt gat gtc tgc gag cct cag tac aag ctc gtc tcg gag
W-->  656 ccc atc acg      749Arg Asp Val Cys Glu Pro Gln Tyr Lys Leu Val Ser Glu Pro Ile
E-->  657 thr      185             190                195                200
W-->  658 tgg aaa ctg ctg ggc atg gga ctc gag ctg ctc ttt ggc ttc ttc atc      797Trp Lys
W-->  659 Leu Leu Gly Met Gly Leu Glu Leu Leu Phe Gly Phe Phe Ile
W-->  660 205             210             215         cct ttg ctg ttt atg gtg
W-->  661 ttc tgt tac ctg ttc atc atc aag acc ttg      845Pro Leu Leu Phe Met Val Phe Cys
E-->  662 tyr Leu Phe Ile Ile Lys thr Leu      220                225
W-->  663 230             gtg cag gcc cag aat tcc aag agg cac aga gcc atc cga gtc gtg
W-->  664 att      893Val Gln Ala Gln Asn Ser Lys Arg His Arg Ala Ile Arg Val Val Ile
W-->  665 235             240             245         gct gtg gtt ctc
```

```
W--> 666 gtg ttc ctg gct tgt cag atc cct cac aac atg gtc      941Ala Val Val Leu Val Phe
E--> 667 Leu ala cys gln Ile Pro his asn met val              250                    255
W--> 668 260                             ctc ctc gtg act gca gcc aac acg ggc aaa atg ggc cgc
W--> 669 agc tgc agc        989Leu Leu Val Thr Ala Ala Asn Thr Gly Lys Met Gly Arg Ser Cys
E--> 670 ser        265                  270               275                    280
W--> 671 gcc gag aaa gcc ctc gcc tac gcc agg aat gtg gct gag gtc ctg gct      1037Ala Glu
W--> 672 Lys Ala Leu Ala Tyr Ala Arg Asn Val Ala Glu Val Leu Ala
W--> 673 285                    290                  295         ttc ctg cac tgc tgt ctc
W--> 674 aac ccc gtg ttg tat gcc ttc att gga cag      1085Phe Leu His Cys Cys Leu Asn Pro
E--> 675 val Leu tyr ala Phe Ile gly gln                        300                    305
W--> 676 310                         aaa ttc aga agc tac ttc atg aag atc atg aag gat gtg tgg tgt
W--> 677 atg       1133Lys Phe Arg Ser Tyr Phe Met Lys Ile Met Lys Asp Val Trp Cys Met
W--> 678 315                    320                  325              agg agg aag agc
W--> 679 aag gtg cct acc ttc ttc tgt gcc cgg gtt tac tca      1181Arg Arg Lys Ser Lys Val
E--> 680 Pro thr Phe Phe cys ala arg val tyr ser              330                    335
W--> 681 340                         gaa agc tac atc tcc agg cag acc agt gag act gta gaa
W--> 682 aat gac aac       1229Glu Ser Tyr Ile Ser Arg Gln Thr Ser Glu Thr Val Glu Asn Asp
E--> 683 asn        345                  350               355                    360
W--> 684 gca tcg tcc ttt acc atg taa cacgagagca caaagcagca tgccccgaaa      1280Ala Ser
W--> 685 Ser Phe Thr Met
W--> 686 365                                             gcctttgtga aacttgctat
E--> 687 tacatgtga                           1309
```

<210> 11
<211> 20
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Oligonucleotide designed to act as primer for amplifying fragment
of rat MIP-3(f¿) gene transcript.

do NOT use scientific symbols or foreign accent marks

(They cannot be processed by CRF software.)

↓ global error

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\09132005\J547532.raw**

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 47,48,49,50,51,52,53,54,55,56,57,59,60,61
Seq#:3; Line(s) 104,105,107,108,109,110,111,112,113,114,115,116,117,118,119
Seq#:5; Line(s) 161,162,163,164,165,166,167,168,169,170,171,172,173,174,175
Seq#:5; Line(s) 176,177
Seq#:7; Line(s) 211,212,213,214,215,216,217,218,219,220,221,222,223,224,225
Seq#:7; Line(s) 226,227,228,229,230,231,232,233,234,235,236,237,238,239,240
Seq#:7; Line(s) 241,242,243,244,245,246,247,248,249,250,251,252,253,254,255
Seq#:7; Line(s) 256,257,258,259,260,261,262,263,264,265,266,267,268,269,270
Seq#:7; Line(s) 271
Seq#:9; Line(s) 340,341,342,343,344,345,346,347,348,349,350,351,352,353,354
Seq#:9; Line(s) 355,356,357,358,359,360,361,362,363,364,365,366,367,368,369
Seq#:9; Line(s) 370,371,372,373,374,375,376,377,378,379,380,381,382,383,384
Seq#:9; Line(s) 385,386,387,388,389,390,391,392,393,394,395,396,397,398
Seq#:13; Line(s) 496,497,498,499,500,501,502,503,504,505,506,507,508,509
Seq#:13; Line(s) 510,511,512,513,514,515,516,517,518,519,520,521,522,523
Seq#:13; Line(s) 524,525,526,527,528,529,530,531,532,533,534,535,536,537
Seq#:13; Line(s) 538,539,540,541,542,543,544,545,546,547,548,549,550,551
Seq#:13; Line(s) 552,553,554,555,556
Seq#:15; Line(s) 625,626,627,628,629,630,631,632,633,634,635,636,637,638
Seq#:15; Line(s) 639,640,641,642,643,644,645,646,647,648,649,650,651,652
Seq#:15; Line(s) 653,654,655,656,657,658,659,660,661,662,663,664,665,666
Seq#:15; Line(s) 667,668,669,670,671,672,673,674,675,676,677,678,679,680
Seq#:15; Line(s) 681,682,683,684,685

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:11,12,16,17,18,19,20,21

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\09132005\J547532.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:41 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:34
L:46 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:39
L:46 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:44
L:47 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:48 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:48 M:254 E: No. of Bases conflict, LENGTH:Input:-25 Counted:43 SEQ:1
L:48 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:17
L:48 M:112 C: (48) String data converted to lower case,
L:49 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:10
L:50 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:50 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:9
L:51 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:25
L:51 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
M:254 Repeated in SeqNo=1
L:51 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5
M:112 Repeated in SeqNo=1
L:52 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:53 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:53 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:54 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:54 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8
L:55 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:55 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:12
M:341 Repeated in SeqNo=1
L:56 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:56 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:13
L:57 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:15
L:58 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:58 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
L:59 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:59 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5
L:60 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:60 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:15
L:61 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:61 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:14
L:62 M:252 E: No. of Seq. differs, <211> LENGTH:Input:288 Found:127 SEQ:1
L:98 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:91
L:103 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:96
L:103 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:101
L:104 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:105 M:254 E: No. of Bases conflict, LENGTH:Input:-25 Counted:43 SEQ:3
L:105 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:20
L:105 M:112 C: (48) String data converted to lower case,
M:254 Repeated in SeqNo=3
L:107 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17

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L:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:109 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:109 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:10
L:110 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:110 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11
L:111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:22
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:111 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:7
M:112 Repeated in SeqNo=3
L:112 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:15
L:113 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:113 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:114 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
L:115 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:115 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:14
M:341 Repeated in SeqNo=3
L:116 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:116 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12
L:117 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:14
L:118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:118 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5
L:119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:119 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:119 M:252 E: No. of Seq. differs, <211> LENGTH:Input:288 Found:106 SEQ:3
L:155 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:148
L:160 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:153
L:160 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:158
L:161 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:162 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:162 M:254 E: No. of Bases conflict, LENGTH:Input:-25 Counted:43 SEQ:5
L:162 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:17
L:162 M:112 C: (48) String data converted to lower case,
L:163 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11
L:164 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:164 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8
L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:25
L:165 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
M:254 Repeated in SeqNo=5
L:165 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
M:112 Repeated in SeqNo=5
L:166 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:167 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:167 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:168 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:168 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:9
L:169 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:169 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11
M:341 Repeated in SeqNo=5
```

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\09132005\J547532.raw**

```
L:170 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:170 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:10
L:171 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:16
L:172 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:172 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:173 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:173 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:174 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:174 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:13
L:175 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:175 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11
L:176 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:177 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:177 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L:177 M:252 E: No. of Seq. differs, <211> LENGTH:Input:291 Found:118 SEQ:5
L:210 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:208
L:211 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:212 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:212 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:42 SEQ:7
L:212 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:15
L:212 M:112 C: (48) String data converted to lower case,
L:213 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:9
L:214 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:214 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11
L:215 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
M:254 Repeated in SeqNo=7
L:215 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
M:112 Repeated in SeqNo=7
L:216 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:16
L:217 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:217 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:218 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:218 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:219 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:219 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:13
M:341 Repeated in SeqNo=7
L:220 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:220 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:14
L:221 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:14
L:222 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:222 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
L:223 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:223 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:224 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17
L:225 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:226 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:226 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:9
L:227 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
```

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L:227 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11
L:228 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:228 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:7
L:229 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:16
L:230 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:230 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:231 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:231 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:232 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:232 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:13
L:233 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:10
L:234 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:14
L:241 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5
L:246 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:17
L:254 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9
L:259 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:7
L:262 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:267 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
L:272 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1122 Found:294 SEQ:7
L:339 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:337
L:341 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:341 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:42 SEQ:9
L:341 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9
L:341 M:112 C: (48) String data converted to lower case,
M:254 Repeated in SeqNo=9
L:344 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9
M:112 Repeated in SeqNo=9
M:341 Repeated in SeqNo=9
L:349 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11
L:352 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:357 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:10
L:362 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11
L:370 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
L:375 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:16
L:378 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:383 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8
L:388 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11
L:391 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:396 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8
L:399 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1101 Found:294 SEQ:9
L:490 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:488
L:491 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:13
M:254 Repeated in SeqNo=13
L:496 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
M:341 Repeated in SeqNo=13
L:497 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
M:112 Repeated in SeqNo=13
L:499 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9
L:502 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
```

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\09132005\J547532.raw**

```
L:507 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11
L:512 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12
L:517 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:16
L:520 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:522 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:15
L:525 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
L:530 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12
L:535 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9
L:557 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1502 Found:528 SEQ:13
L:622 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:620
L:623 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:15
M:254 Repeated in SeqNo=15
M:341 Repeated in SeqNo=15
M:112 Repeated in SeqNo=15
L:687 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1309 Found:470 SEQ:15
```